

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO:1:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1277 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 10 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 15 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1275  
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC 48  
 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile  
 1 5 10 15  
 25 TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC 96  
 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly  
 20 25 30  
 30 ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG 144  
 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys  
 35 40 45  
 35 CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA 192  
 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg  
 50 55 60  
 40 TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC 240  
 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr  
 65 70 75 80  
 CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA 288  
 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly  
 85 90 95  
 45 GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG 336  
 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu  
 100 105 110  
 50 GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC 384  
 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr  
 115 120 125  
 55 GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC 432  
 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr  
 130 135 140  
 GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG 480  
 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys  
 145 150 155 160

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	TAC	GGA	ATG	CTG	GCC	CGC	CTC	GCC	GTC	GAG	GCC	GGC	TTC	GAC	TGG	GTC	528
	Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
					165					170					175		
5	TAC	TAC	GAG	TCC	AAG	GCG	CAC	ATC	CAC	TGC	TCC	GTC	AAA	GCA	GAA	AAC	576
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	
				180					185					190			
10	TCA	GTG	GCA	GCG	AAA	TCA	GGA	GGC	TGC	TTC	CCT	GGC	TCA	GCC	ACA	GTG	624
	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	
			195					200					205				
15	CAC	CTG	GAG	CAT	GGA	GGC	ACC	AAG	CTG	GTG	AAG	GAC	CTG	AGC	CCT	GGG	672
	His	Leu	Glu	His	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	
			210					215					220				
20	GAC	CGC	GTG	CTG	GCT	GCT	GAC	GCG	GAC	GGC	CGG	CTG	CTC	TAC	AGT	GAC	720
	Asp	Arg	Val	Leu	Ala	Ala	Asp	Ala	Asp	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	
						230					235					240	
25	TTC	CTC	ACC	TTC	CTC	GAC	CGG	ATG	GAC	AGC	TCC	CGA	AAG	CTC	TTC	TAC	768
	Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr	
					245						250					255	
30	GTC	ATC	GAG	ACG	CGG	CAG	CCC	CGG	GCC	CGG	CTG	CTA	CTG	ACG	GCG	GCC	816
	Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Leu	Thr	Ala	Ala	
				260						265				270			
35	CAC	CTG	CTC	TTT	GTG	GCC	CCC	CAG	CAC	AAC	CAG	TCG	GAG	GCC	ACA	GGG	864
	His	Leu	Leu	Phe	Val	Ala	Pro	Gln	His	Asn	Gln	Ser	Glu	Ala	Thr	Gly	
				275				280						285			
40	TCC	ACC	AGT	GGC	CAG	GCG	CTC	TTC	GCC	AGC	AAC	GTG	AAG	CCT	GGC	CAA	912
	Ser	Thr	Ser	Gly	Gln	Ala	Leu	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Gln	
				290			295					300					
45	CGT	GTC	TAT	GTG	CTG	GGC	GAG	GGC	GGG	CAG	CAG	CTG	CTG	CCG	GCG	TCT	960
	Arg	Val	Tyr	Val	Leu	Gly	Glu	Gly	Gly	Gln	Gln	Leu	Leu	Pro	Ala	Ser	
					310						315					320	
50	GTC	CAC	AGC	GTC	TCA	TTG	CGG	GAG	GAG	GCG	TCC	GGA	GCC	TAC	GCC	CCA	1008
	Val	His	Ser	Val	Ser	Leu	Arg	Glu	Glu	Ala	Ser	Gly	Ala	Tyr	Ala	Pro	
					325					330					335		
55	CTC	ACC	GCC	CAG	GGC	ACC	ATC	CTC	ATC	AAC	CGG	GTG	TTG	GCC	TCC	TGC	1056
	Leu	Thr	Ala	Gln	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	
				340				345						350			
60	TAC	GCC	GTC	ATC	GAG	GAG	CAC	AGT	TGG	GCC	CAT	TGG	GCC	TTC	GCA	CCA	1104
	Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro	
				355				360					365				
65	TTC	CGC	TTG	GCT	CAG	GGG	CTG	CTG	GCC	GCC	CTC	TGC	CCA	GAT	GGG	GCC	1152
	Phe	Arg	Leu	Ala	Gln	Gly	Leu	Leu	Ala	Ala	Leu	Cys	Pro	Asp	Gly	Ala	
				370			375					380					
70	ATC	CCT	ACT	GCC	GCC	ACC	ACC	ACC	ACT	GGC	ATC	CAT	TGG	TAC	TCA	CGG	1200
	Ile	Pro	Thr	Ala	Ala	Thr	Thr	Thr	Thr	Gly	Ile	His	Trp	Tyr	Ser	Arg	
						390					395					400	
75	CTC	CTC	TAC	CGC	ATC	GGC	AGC	TGG	GTG	CTG	GAT	GGT	GAC	GCG	CTG	CAT	1248
	Leu	Leu	Tyr	Arg	Ile	Gly	Ser	Trp	Val	Leu	Asp	Gly	Asp	Ala	Leu	His	

	405	410	415	
	CCG CTG GGC ATG GTG GCA CCG GCC AGC TG			1277
5	Pro Leu Gly Met Val Ala Pro Ala Ser			
	420	425		

(2) INFORMATION FOR SEQ ID NO:2:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1190 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

20 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1191

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG	48
	Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	
	1 5 10 15	
30	GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG	96
	Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	
	20 25 30	
35	CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT	144
	Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	
	35 40 45	
40	GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG	192
	Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	
	50 55 60	
45	GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC	240
	Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	
	65 70 75 80	
50	TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC	288
	Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	
	85 90 95	
55	CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC	336
	Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	
	100 105 110	
60	GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC	384
	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
	115 120 125	
60	TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC	432
	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
	130 135 140	

5	CGT	GCC	TTG	GAC	ATC	ACC	ACG	TCT	GAC	CGT	GAC	CGT	AAT	AAG	TAT	GGT	480
	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
10	TTG	TTG	GCG	CGC	CTA	GCT	GTG	GAA	GCC	GGA	TTC	GAC	TGG	GTC	TAC	TAC	528
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
15	GAG	TCC	CGC	AAC	CAC	ATC	CAC	GTA	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
20	GCG	GTC	CGA	GCC	GGA	GGC	TGC	TTT	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTG	624
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
25	CGG	AGC	GGC	GAA	CGG	AAG	GGG	CTG	AGG	GAA	CTA	CAT	CGT	GGT	GAC	TGG	672
	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
30	GTA	CTG	GCC	GCT	GAT	GCA	GCG	GGC	CGA	GTG	GTA	CCC	ACG	CCA	GTG	CTG	720
	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
35	CTC	TTC	CTG	GAC	CGG	GAT	CTG	CAG	CGC	CGC	GCC	TCG	TTC	GTG	GCT	GTG	768
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
40	GAG	ACC	GAG	CGG	CCT	CCG	CGC	AAA	CTG	TTG	CTC	ACA	CCC	TGG	CAT	CTG	816
	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
45	GTG	TTC	GCT	GCT	CGC	GGG	CCA	GCG	CCT	GCT	CCA	GGT	GAC	TTT	GCA	CCG	864
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
50	GTG	TTC	GCG	CGC	CGC	TTA	CGT	GCT	GGC	GAC	TCG	GTG	CTG	GCT	CCC	GGC	912
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	
55	GGG	GAC	GCG	CTC	CAG	CCG	GCG	CGC	GTA	GCC	CGC	GTG	GCG	CGC	GAG	GAA	960
	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu	
60	GCC	GTG	GGC	GTG	TTC	GCA	CCG	CTC	ACT	GCG	CAC	GGG	ACG	CTG	CTG	GTC	1008
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val	
65	AAC	GAC	GTC	CTC	GCC	TCC	TGC	TAC	GCG	GTT	CTA	GAG	AGT	CAC	CAG	TGG	1056
	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp	
70	GCC	CAC	CGC	GCC	TTC	GCC	CCT	TTG	CGG	CTG	CTG	CAC	GCG	CTC	GGG	GCT	1104
	Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala	
75	CTG	CTC	CCT	GGG	GGT	GCA	GTC	CAG	CCG	ACT	GGC	ATG	CAT	TGG	TAC	TCT	1152
	Leu	Leu	Pro	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser	

CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG 1190  
Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly  
385 390 395

5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 20 (A) NAME/KEY: CDS  
(B) LOCATION: 1..1233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25 ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG 48  
Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu  
1 5 10 15

30 CTG CTG CTG CTT CTG GTG CCG GCG GCG CGG GGC TGC GGG CCG GGC CGG 96  
Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg  
20 25 30

35 GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC 144  
Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala  
35 40 45

40 TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC 192  
Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser  
50 55 60

45 GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG 240  
Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu  
65 70 75 80

50 CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC 288  
Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn  
85 90 95

55 ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC 336  
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn  
100 105 110

60 TCA CTG GCC ATC TCT GTC ATG AAC CAG TGG CCT GGT GTG AAA CTG CGG 384  
Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg  
115 120 125

65 GTG ACC GAA GGC CGG GAT GAA GAT GGC CAT CAC TCA GAG GAG TCT TTA 432  
Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu  
130 135 140

70 CAC TAT GAG GGC CGC GCG GTG GAT ATC ACC ACC TCA GAC CGT GAC CGA 480  
His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg

	145				150				155				160				
5	AAT	AAG	TAT	GGA	CTG	GCG	CGC	TTA	GCA	GTG	GAG	GCC	GGC	TTC	GAC	528	
	Asn	Lys	Tyr	Gly	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp		
10	TGG	GTG	TAT	TAC	GAG	TCC	AAG	GCC	CAC	GTG	CAT	TGC	TCT	GTC	AAG	TCT	576
	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	
15	GAG	CAT	TCG	GCC	GCT	GCC	AAG	ACA	GGT	GGC	TGC	TTT	CCT	GCC	GGA	GCC	624
	Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
20	CAG	GTG	CGC	CTA	GAG	AAC	GGG	GAG	CGT	GTG	GCC	CTG	TCA	GCT	GTA	AAG	672
	Gln	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys	
25	CCA	GGA	GAC	CGG	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	ACC	CCC	ACC	TTC	720
	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
30	AGT	GAT	GTG	CTT	ATT	TTC	CTG	GAC	CGC	GAG	CCA	AAC	CGG	CTG	AGA	GCT	768
	Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	
35	TTC	CAG	GTC	ATC	GAG	ACT	CAG	GAT	CCT	CCG	CGT	CGG	CTG	GCG	CTC	ACG	816
	Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
40	CCT	GCC	CAC	CTG	CTC	TTC	ATT	GCG	GAC	AAT	CAT	ACA	GAA	CCA	GCA	GCC	864
	Pro	Ala	His	Leu	Leu	Phe	Ile	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	
45	CAC	TTC	CGG	GCC	ACA	TTT	GCC	AGC	CAT	GTG	CAA	CCA	GGC	CAA	TAT	GTG	912
	His	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	
50	CTG	GTA	TCA	GGG	GTA	CCA	GGC	CTC	CAG	CCT	GCT	CGG	GTG	GCA	GCT	GTC	960
	Leu	Val	Ser	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	
55	TCC	ACC	CAC	GTG	GCC	CTT	GGG	TCC	TAT	GCT	CCT	CTC	ACA	AGG	CAT	GGG	1008
	Ser	Thr	His	Val	Ala	Leu	Gly	Ser	Tyr	Ala	Pro	Leu	Thr	Arg	His	Gly	
60	ACA	CTT	GTG	GTG	GAG	GAT	GTG	GTG	GCC	TCC	TGC	TTT	GCA	GCT	GTG	GCT	1056
	Thr	Leu	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	
65	GAC	CAC	CAT	CTG	GCT	CAG	TTG	GCC	TTC	TGG	CCC	CTG	CGA	CTG	TTT	CCC	1104
	Asp	His	His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	Pro	
70	AGT	TTG	GCA	TGG	GGC	AGC	TGG	ACC	CCA	AGT	GAG	GGT	GTT	CAC	TCC	TAC	1152
	Ser	Leu	Ala	Trp	Gly	Ser	Trp	Thr	Pro	Ser	Glu	Gly	Val	His	Ser	Tyr	
75	CCT	CAG	ATG	CTC	TAC	CGC	CTG	GGG	CGT	CTC	TTG	CTA	GAA	GAG	AGC	ACC	1200
	Pro	Gln	Met	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Glu	Glu	Ser	Thr		

TTC CAT CCA CTG GGC ATG TCT GGG GCA GGA AGC TGAAGGGACT CTAACCACTG 1253  
Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser  
405 410

5

CCCTCCTGGA ACTGCTGTGC GTGGATCC 1281

(2) INFORMATION FOR SEQ ID NO:4:

10

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1313 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

20

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..1314

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG CTG CTG CTG CTG GCC AGA TGT TTT CTG GTG ATC CTT GCT TCC TCG 48  
Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser  
1 5 10 15

30

CTG CTG GTG TGC CCC GGG CTG GCC TGT GGG CCC GGC AGG GGG TTT GGA 96  
Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly  
20 25 30

35

AAG AGG CGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT 144  
Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe  
35 40 45

40

ATT CCC AAC GTA GCC GAG AAG ACC CTA GGG GCC AGC GGC AGA TAT GAA 192  
Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu  
50 55 60

45

GGG AAG ATC ACA AGA AAC TCC GAA CGA TTT AAG GAA CTC ACC CCC AAT 240  
Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn  
65 70 75 80

50

TAC AAC CCC GAC ATC ATA TTT AAG GAT GAG GAA AAC ACG GGA GCA GAC 288  
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp  
85 90 95

55

CGG CTG ATG ACT CAG AGG TGC AAA GAC AAG TTA AAT GCC TTG GCC ATC 336  
Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile  
100 105 110

60

TCT GTG ATG AAC CAG TGG CCT GGA GTG AGG CTG CGA GTG ACC GAG GGC 384  
Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly  
115 120 125

TGG GAT GAG GAC GGC CAT CAT TCA GAG GAG TCT CTA CAC TAT GAG GGT 432  
Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly  
130 135 140

	CGA Arg 145	GCA Ala	GTG Val	GAC Asp	ATC Ile	ACC Thr 150	ACG Thr	TCC Ser	GAC Asp	CGG Arg	GAC Asp 155	CGC Arg	AGC Ser	AAG Lys	TAC Tyr	GGC Gly 160	480
5	ATG Met	CTG Leu	GCT Ala	CGC Arg	CTG Leu 165	GCT Ala	GTG Val	GAA Glu	GCA Ala	GGT Gly 170	TTC Phe	GAC Asp	TGG Trp	GTC Val	TAC Tyr 175	TAT Tyr	528
10	GAA Glu	TCC Ser	AAA Lys	GCT Ala 180	CAC His	ATC Ile	CAC His	TGT Cys	TCT Ser 185	GTG Val	AAA Lys	GCA Ala	GAG Glu	AAC Asn 190	TCC Ser	GTG Val	576
15	GCG Ala	GCC Ala	AAA Lys 195	TCC Ser	GGC Gly	GGC Gly	TGT Cys	TTC Phe 200	CCG Pro	GGA Gly	TCC Ser	GCC Ala	ACC Thr 205	GTG Val	CAC His	CTG Leu	624
20	GAG Glu	CAG Gln 210	GGC Gly	GGC Gly	ACC Thr	AAG Lys	CTG Leu 215	GTG Val	AAG Lys	GAC Asp	TTA Leu 220	CGT Arg	CCC Pro	GGA Gly	GAC Asp	CGC Arg	672
25	GTG Val 225	CTG Leu	GCG Ala	GCT Ala	GAC Asp	GAC Asp 230	CAG Gln	GGC Gly	CGG Arg	CTG Leu	CTG Leu 235	TAC Tyr	AGC Ser	GAC Asp	TTC Phe	CTC Leu 240	720
	ACC Thr	TTC Phe	CTG Leu	GAC Asp	CGC Arg 245	GAC Asp	GAA Glu	GGC Gly	GCC Ala	AAG Lys 250	AAG Lys	GTC Val	TTC Phe	TAC Tyr	GTG Val 255	ATC Ile	768
30	GAG Glu	ACG Thr	CTG Leu	GAG Glu 260	CCG Pro	CGC Arg	GAG Glu	CGC Arg	CTG Leu 265	CTG Leu	CTC Leu	ACC Thr	GCC Ala	GCG Ala 270	CAC His	CTG Leu	816
35	CTC Leu	TTC Phe	GTG Val 275	GCG Ala	CCG Pro	CAC His	AAC Asn	GAC Asp 280	TCG Ser	GGG Gly	CCC Pro	ACG Thr	CCC Pro 285	GGG Gly	CCA Pro	AGC Ser	864
40	GCG Ala 290	CTC Leu	TTT Phe	GCC Ala	AGC Ser	CGC Arg	GTG Val 295	CGC Arg	CCC Pro	GGG Gly	CAG Gln 300	CGC Arg	GTG Val	TAC Tyr	GTG Val	GTG Val	912
45	GCT Ala 305	GAA Glu	CGC Arg	GGC Gly	GGG Gly	GAC Asp 310	CGC Arg	CGG Arg	CTG Leu	CTG Leu	CCC Pro 315	GCC Ala	GCG Ala	GTG Val	CAC His	AGC Ser 320	960
	GTG Val	ACG Thr	CTG Leu	CGA Arg 325	GAG Glu	GAG Glu	GAG Glu	GCG Ala	GGC Gly 330	GCG Ala	TAC Tyr	GCG Ala	CCG Pro	CTC Leu	ACG Thr 335	GCG Ala	1008
50	CAC His	GGC Gly	ACC Thr	ATT Ile 340	CTC Leu	ATC Ile	AAC Asn	CGG Arg	GTG Val 345	CTC Leu	GCC Ala	TCG Ser	TGC Cys	TAC Tyr 350	GCT Ala	GTC Val	1056
55	ATC Ile	GAG Glu	GAG Glu 355	CAC His	AGC Ser	TGG Trp	GCA Ala	CAC His 360	CGG Arg	GCC Ala	TTC Phe	GCG Ala	CCT Pro 365	TTC Phe	CGC Arg	CTG Leu	1104
60	GCG Ala 370	CAC His	GCG Ala	CTG Leu	CTG Leu	GCC Ala	GCG Ala 375	CTG Leu	GCA Ala	CCC Pro	GCC Ala	CGC Arg 380	ACG Thr	GAC Asp	GGC Gly	GGG Gly	1152



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	100								105				110							
5	GTA	ATG	AAC	CAC	TGG	CCA	GGG	GTT	AAG	CTG	CGT	GTG	ACA	GAG	GGC	TGG	384			
	Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp				
	115						120			125										
10	GAT	GAG	GAC	GGT	CAC	CAT	TTT	GAA	GAA	TCA	CTC	CAC	TAC	GAG	GGA	AGA	432			
	Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg				
	130						135			140										
15	GCT	GTT	GAT	ATT	ACC	ACC	TCT	GAC	CGA	GAC	AAG	AGC	AAA	TAC	GGG	ACA	480			
	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr				
	145			150			155			160										
20	CTG	TCT	CGC	CTA	GCT	GTG	GAG	GCT	GGA	TTT	GAC	TGG	GTC	TAT	TAC	GAG	528			
	Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu				
				165			170			175										
25	TCC	AAA	GCC	CAC	ATT	CAT	TGC	TCT	GTC	AAA	GCA	GAA	AAT	TCG	GTT	GCT	576			
	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala				
				180			185			190										
30	GCG	AAA	TCT	GGG	GGC	TGT	TTC	CCA	GGT	TCG	GCT	CTG	GTC	TCG	CTC	CAG	624			
	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Leu	Val	Ser	Leu	Gln				
	195						200			205										
35	GAC	GGA	GGA	CAG	AAG	GCC	GTG	AAG	GAC	CTG	AAC	CCC	GGA	GAC	AAG	GTG	672			
	Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val				
	210						215			220										
40	CTG	GCG	GCA	GAC	AGC	GCG	GGA	AAC	CTG	GTG	TTC	AGC	GAC	TTC	ATC	ATG	720			
	Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met				
	225			230			235			240										
45	TTC	ACA	GAC	CGA	GAC	TCC	ACG	ACG	CGA	CGT	GTG	TTT	TAC	GTC	ATA	GAA	768			
	Phe	Thr	Asp	Arg	Asp	Ser	Thr	Thr	Arg	Arg	Val	Phe	Tyr	Val	Ile	Glu				
				245			250			255										
50	ACG	CAA	GAA	CCC	GTT	GAA	AAG	ATC	ACC	CTC	ACC	GCC	GCT	CAC	CTC	CTT	816			
	Thr	Gln	Glu	Pro	Val	Glu	Lys	Ile	Thr	Leu	Thr	Ala	Ala	His	Leu	Leu				
				260			265			270										
55	TTT	GTC	CTC	GAC	AAC	TCA	ACG	GAA	GAT	CTC	CAC	ACC	ATG	ACC	GCC	GCG	864			
	Phe	Val	Leu	Asp	Asn	Ser	Thr	Glu	Asp	Leu	His	Thr	Met	Thr	Ala	Ala				
	275						280			285										
60	TAT	GCC	AGC	AGT	GTC	AGA	GCC	GGA	CAA	AAG	GTG	ATG	GTT	GTT	GAT	GAT	912			
	Tyr	Ala	Ser	Ser	Val	Arg	Ala	Gly	Gln	Lys	Val	Met	Val	Val	Asp	Asp				
	290						295			300										
65	AGC	GGT	CAG	CTT	AAA	TCT	GTC	ATC	GTG	CAG	CGG	ATA	TAC	ACG	GAG	GAG	960			
	Ser	Gly	Gln	Leu	Lys	Ser	Val	Ile	Val	Gln	Arg	Ile	Tyr	Thr	Glu	Glu				
	305			310			315			320										
70	CAG	CGG	GGC	TCG	TTC	GCA	CCA	GTG	ACT	GCA	CAT	GGG	ACC	ATT	GTG	GTC	1008			
	Gln	Arg	Gly	Ser	Phe	Ala	Pro	Val	Thr	Ala	His	Gly	Thr	Ile	Val	Val				
				325			330			335										
75	GAC	AGA	ATA	CTG	GCG	TCC	TGT	TAC	GCC	GTA	ATA	GAG	GAC	CAG	GGG	CTT	1056			
	Asp	Arg	Ile	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	Asp	Gln	Gly	Leu				
				340			345			350										

5 GCG CAT TTG GCC TTC GCG CCC GCC AGG CTC TAT TAT TAC GTG TCA TCA 1104  
Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser  
355 360 365

10 TTC CTG TCC CCC AAA ACT CCA GCA GTC GGT CCA ATG CGA CTT TAC AAC 1152  
Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn  
370 375 380

15 AGG AGG GGG TCC ACT GGT ACT CCA GGC TCC TGT CAT CAA ATG GGA ACG 1200  
Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr  
385 390 395 400

20 TGG CTT TTG GAC AGC AAC ATG CTT CAT CCT TTG GGG ATG TCA GTA AAC 1248  
Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn  
405 410 415

TCA AGC TG 1256  
Ser Ser

(2) INFORMATION FOR SEQ ID NO:6:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1425 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

35 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..1425

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG CTG CTG CTG GCG AGA TGT CTG CTG CTA GTC CTC GTC TCC TCG CTG 48  
Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu  
1 5 10 15

45 CTG GTA TGC TCG GGA CTG GCG TGC GGA CCG GGC AGG GGG TTC GGG AAG 96  
Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys  
20 25 30

50 AGG AGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT ATC 144  
Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile  
35 40 45

55 CCC AAT GTG GCC GAG AAG ACC CTA GGC GCC AGC GGA AGG TAT GAA GGG 192  
Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly  
50 55 60

60 AAG ATC TCC AGA AAC TCC GAG CGA TTT AAG GAA CTC ACC CCC AAT TAC 240  
Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr  
65 70 75 80

AAC CCC GAC ATC ATA TTT AAG GAT GAA GAA AAC ACC GGA GCG GAC AGG 288

	Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg	
5	CTG Leu	ATG Met	ACT Thr	CAG Gln 100	AGG Arg	TGT Cys	AAG Lys	GAC Asp	AAG Lys 105	TTG Leu	AAC Asn	GCT Ala	TTG Leu	GCC Ala 110	ATC Ile	TCG Ser	336
10	GTG Val	ATG Met	AAC Asn 115	CAG Gln	TGG Trp	CCA Pro	GGA Gly	GTG Val 120	AAA Lys	CTG Leu	CGG Arg	GTG Val	ACC Thr 125	GAG Glu	GGC Gly	TGG Trp	384
15	GAC Asp	GAA Glu 130	GAT Asp	GGC Gly	CAC His	CAC His	TCA Ser 135	GAG Glu	GAG Glu	TCT Ser	CTG Leu	CAC His 140	TAC Tyr	GAG Glu	GGC Gly	CGC Arg	432
20	GCA Ala 145	GTG Val	GAC Asp	ATC Ile	ACC Thr	ACG Thr 150	TCT Ser	GAC Asp	CGC Arg	GAC Asp 155	CGC Arg	AGC Ser	AAG Lys	TAC Tyr	GGC Gly	ATG Met 160	480
25	CTG Leu	GCC Ala	CGC Arg	CTG Leu	GCG Ala 165	GTG Val	GAG Glu	GCC Ala	GGC Gly 170	TTC Phe	GAC Asp	TGG Trp	GTG Val	TAC Tyr	TAC Tyr 175	GAG Glu	528
30	TCC Ser	AAG Lys	GCA Ala	CAT His 180	ATC Ile	CAC His	TGC Cys	TCG Ser	GTG Val 185	AAA Lys	GCA Ala	GAG Glu	AAC Asn	TCG Ser 190	GTG Val	GCG Ala	576
35	GCC Ala	AAA Lys	TCG Ser 195	GGA Gly	GGC Gly	TGC Cys	TTC Phe 200	CCG Pro	GGC Gly	TCG Ser	GCC Ala	ACG Thr	GTG Val 205	CAC His	CTG Leu	GAG Glu	624
40	CAG Gln 210	GGC Gly	GGC Gly	ACC Thr	AAG Lys	CTG Leu	GTG Val 215	AAG Lys	GAC Asp	CTG Leu	AGC Ser	CCC Pro 220	GGG Gly	GAC Asp	CGC Arg	GTG Val	672
45	CTG Leu 225	GCG Ala	GCG Ala	GAC Asp	GAC Asp	CAG Gln 230	GGC Gly	CGG Arg	CTG Leu	CTC Leu	TAC Tyr 235	AGC Ser	GAC Asp	TTC Phe	CTC Leu	ACT Thr 240	720
50	TTC Phe	CTG Leu	GAC Asp	CGC Arg	GAC Asp 245	GAC Asp	GGC Gly	GCC Ala	AAG Lys	AAG Lys 250	GTC Val	TTC Phe	TAC Tyr	GTG Val	ATC Ile 255	GAG Glu	768
55	ACG Thr	CGG Arg	GAG Glu	CCG Pro 260	CGC Arg	GAG Glu	CGC Arg	CTG Leu	CTG Leu 265	CTC Leu	ACC Thr	GCC Ala	GCG Ala 270	CAC His	CTG Leu	CTC Leu	816
60	TTT Phe	GTG Val	GCG Ala 275	CCG Pro	CAC His	AAC Asn	GAC Asp	TCG Ser 280	GCC Ala	ACC Thr	GGG Gly	GAG Glu	CCC Pro 285	GAG Glu	GCG Ala	TCC Ser	864
65	TCG Ser	GGC Gly 290	TCG Ser	GGG Gly	CCG Pro	CCT Pro	TCC Ser 295	GGG Gly	GGC Gly	GCA Ala	CTG Leu	GGG Gly 300	CCT Pro	CGG Arg	GCG Ala	CTG Leu	912
70	TTC Phe 305	GCC Ala	AGC Ser	CGC Arg	GTG Val	CGC Arg 310	CCG Pro	GGC Gly	CAG Gln	CGC Arg	GTG Val 315	TAC Tyr	GTG Val	GTG Val	GCC Ala	GAG Glu 320	960
75	CGT Arg	GAC Asp	GGG Gly	GAC Asp	CGC Arg	CGG Arg	CTC Leu	CTG Leu	CCC Pro	GCC Ala	GCT Ala	GTG Val	CAC His	AGC Ser	GTG Val	ACC Thr	1008

	325	330	335		
5	CTA AGC GAG GAG GCC GCG GGC GCC TAC GCG CCG CTC ACG GCC CAG GGC Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly	340	345	350	1056
10	ACC ATT CTC ATC AAC CGG GTG CTG GCC TCG TGC TAC GCG GTC ATC GAG Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu	355	360	365	1104
15	GAG CAC AGC TGG GCG CAC CGG GCC TTC GCG CCC TTC CGC CTG GCG CAC Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His	370	375	380	1152
20	GCG CTC CTG GCT GCA CTG GCG CCC GCG CGC ACG GAC CGC GGC GGC GAC Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp	385	390	395	1200
25	AGC GGC GGC GGG GAC CGC GGG GGC GGC GGC GGC AGA GTA GCC CTA ACC Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Arg Val Ala Leu Thr	405	410	415	1248
30	GCT CCA GGT GCT GCC GAC GCT CCG GGT GCG GGG GCC ACC GCG GGC ATC Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile	420	425	430	1296
35	CAC TGG TAC TCG CAG CTG CTC TAC CAA ATA GGC ACC TGG CTC CTG GAC His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp	435	440	445	1344
40	AGC GAG GCC CTG CAC CCG CTG GGC ATG GCG GTC AAG TCC AGC NNN AGC Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser	450	455	460	1392
45	CGG GGG GCC GGG GGA GGG GCG CGG GAG GGG GCC Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala	465	470	475	1425

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 51..1283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CATCAGCCCA	CCAGGAGACC	TCGCCCCCGG	CTCCCCCGGG	CTCCCCGGCC	ATG TCT	56
					Met Ser	
					1	

105044-012350

	CCC	GCC	CGG	CTC	CGG	CCC	CGA	CTG	CAC	TTC	TGC	CTG	GTC	CTG	TTG	CTG	104
	Pro	Ala	Arg	Leu	Arg	Pro	Arg	Leu	His	Phe	Cys	Leu	Val	Leu	Leu	Leu	
5			5					10					15				
	CTG	CTG	GTG	GTG	CCC	GCG	GCA	TGG	GGC	TGC	GGG	CCG	GGT	CGG	GTG	GTG	152
	Leu	Leu	Val	Val	Pro	Ala	Ala	Trp	Gly	Cys	Gly	Pro	Gly	Arg	Val	Val	
		20					25					30					
10	GGC	AGC	CGC	CGG	CGA	CCG	CCA	CGC	AAA	CTC	GTG	CCG	CTC	GCC	TAC	AAG	200
	Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala	Tyr	Lys	
	35					40					45					50	
15	CAG	TTC	AGC	CCC	AAT	GTG	CCC	GAG	AAG	ACC	CTG	GGC	GCC	AGC	GGA	CGC	248
	Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	
					55					60					65		
20	TAT	GAA	GGC	AAG	ATC	GCT	CGC	AGC	TCC	GAG	CGC	TTC	AAG	GAG	CTC	ACC	296
	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	
				70					75					80			
25	CCC	AAT	TAC	AAT	CCA	GAC	ATC	ATC	TTC	AAG	GAC	GAG	GAG	AAC	ACA	GGC	344
	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	
			85					90					95				
	GCC	GAC	CGC	CTC	ATG	ACC	CAG	CGC	TGC	AAG	GAC	CGC	CTG	AAC	TCG	CTG	392
	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	Ser	Leu	
		100					105					110					
30	GCT	ATC	TCG	GTG	ATG	AAC	CAG	TGG	CCC	GGT	GTG	AAG	CTG	CGG	GTG	ACC	440
	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
	115					120					125					130	
35	GAG	GGC	TGG	GAC	GAG	GAC	GGC	CAC	CAC	TCA	GAG	GAG	TCC	CTG	CAT	TAT	488
	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	
					135					140					145		
40	GAG	GGC	CGC	GCG	GTG	GAC	ATC	ACC	ACA	TCA	GAC	CGC	GAC	CGC	AAT	AAG	536
	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	
				150					155					160			
45	TAT	GGA	CTG	CTG	GCG	CGC	TTG	GCA	GTG	GAG	GCC	GGC	TTT	GAC	TGG	GTG	584
	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
			165				170						175				
	TAT	TAC	GAG	TCA	AAG	GCC	CAC	GTG	CAT	TGC	TCC	GTC	AAG	TCC	GAG	CAC	632
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	Glu	His	
		180					185					190					
50	TCG	GCC	GCA	GCC	AAG	ACG	GGC	GGC	TGC	TTC	CCT	GCC	GGA	GCC	CAG	GTA	680
	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	Gln	Val	
	195					200					205				210		
55	CGC	CTG	GAG	AGT	GGG	GCG	CGT	GTG	GCC	TTG	TCA	GCC	GTG	AGG	CCG	GGA	728
	Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	Pro	Gly	
					215					220					225		
60	GAC	CGT	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	AGC	CCC	ACC	TTC	AGC	GAT	776
	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe	Ser	Asp	
				230					235					240			

	GTG	CTC	ATT	TTC	CTG	GAC	CGC	GAG	CCC	CAC	AGG	CTG	AGA	GCC	TTC	CAG	824
	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala	Phe	Gln	
			245					250					255				
5	GTC	ATC	GAG	ACT	CAG	GAC	CCC	CCA	CGC	CGC	CTG	GCA	CTC	ACA	CCC	GCT	872
	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	GCA	Ala	Leu	Thr	Pro	
			260				265					270					
10	CAC	CTG	CTC	TTT	ACG	GCT	GAC	AAT	CAC	ACG	GAG	CCG	GCA	GCC	CGC	TTC	920
	His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	Arg	Phe	
						280					285					290	
15	CGG	GCC	ACA	TTT	GCC	AGC	CAC	GTG	CAG	CCT	GGC	CAG	TAC	GTG	CTG	GTG	968
	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	Leu	Val	
					295					300					305		
20	GCT	GGG	GTG	CCA	GGC	CTG	CAG	CCT	GCC	CGC	GTG	GCA	GCT	GTC	TCT	ACA	1016
	Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	Ser	Thr	
				310				315						320			
25	CAC	GTG	GCC	CTC	GGG	GCC	TAC	GCC	CCG	CTC	ACA	AAG	CAT	GGG	ACA	CTG	1064
	His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly	Thr	Leu	
			325					330					335				
30	GTG	GTG	GAG	GAT	GTG	GTG	GCA	TCC	TGC	TTC	GCG	GCC	GTG	GCT	GAC	CAC	1112
	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	Asp	His	
			340				345					350					
35	CAC	CTG	GCT	CAG	TTG	GCC	TTC	TGG	CCC	CTG	AGA	CTC	TTT	CAC	AGC	TTG	1160
	His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His	Ser	Leu	
					360					365						370	
40	GCA	TGG	GGC	AGC	TGG	ACC	CCG	GGG	GAG	GGT	GTG	CAT	TGG	TAC	CCC	CAG	1208
	Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr	Pro	Gln	
				375				380							385		
45	CTG	CTC	TAC	CGC	CTG	GGG	CGT	CTC	CTG	CTA	GAA	GAG	GGC	AGC	TTC	CAC	1256
	Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser	Phe	His	
				390				395						400			
50	CCA	CTG	GGC	ATG	TCC	GGG	GCA	GGG	AGC	TGAAAGGACT	CCACCGCTGC						1303
	Pro	Leu	Gly	Met	Ser	Gly	Ala	Gly	Ser								
			405				410										
55	CCTCCTGGAA	CTGCTGTACT	GGGTCCAGAA	GCCTCTCAGC	CAGGAGGGAG	CTGGCCCTGG											1363
	AAGGGACCTG	AGCTGGGGGA	CACTGGCTCC	TGCCATCTCC	TCTGCCATGA	AGATACACCA											1423
	TTGAGACTTG	ACTGGGCAAC	ACCAGCGTCC	CCCACCCGCG	TCGTGGTGTA	GTCATAGAGC											1483
	TGCAAGCTGA	GCTGGCGAGG	GGATGGTTGT	TGACCCCTCT	CTCCTAGAGA	CCTTGAGGCT											1543
	GGCAGGCGA	CTCCCACTC	AGCCTGCTCT	CACTACGAGT	TTTCATACTC	TGCCTCCCCC											1603
	ATTGGGAGGG	CCCATCCCC															1622

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

15	ATG GCT CTC CTG ACC AAT CTA CTG CCC TTG TGC TGC TTG GCA CTT CTG	48
	Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	
	1 5 10 15	
20	GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG	96
	Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	
	20 25 30	
25	CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT	144
	Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	
	35 40 45	
30	GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG	192
	Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	
	50 55 60	
35	GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC	240
	Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	
	65 70 75 80	
40	TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC	288
	Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	
	85 90 95	
45	CGC CTG ATG ACC GAG CGT TGC AAG GAG AGG GTG AAC GCT TTG GCC ATT	336
	Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	
	100 105 110	
50	GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC	384
	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
	115 120 125	
55	TGG GAC GAG GAC GGC CAC CAC GCT CAG GAT TCA CTC CAC TAC GAA GGC	432
	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
	130 135 140	
60	CGT GCT TTG GAC ATC ACT ACG TCT GAC CGC GAC CGC AAC AAG TAT GGG	480
	Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
	145 150 155 160	
65	TTG CTG GCG CGC CTC GCA GTG GAA GCC GGC TTC GAC TGG GTC TAC TAC	528
	Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
	165 170 175	
70	GAG TCC CGC AAC CAC GTC CAC GTG TCG GTC AAA GCT GAT AAC TCA CTG	576
	Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	
	180 185 190	



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(ii) MOLECULE TYPE: cDNA

5 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..1248

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GAC GTA AGG CTG CAT CTG AAG CAA TTT GCT TTA CTG TGT TTT ATC	48
Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile	
1 5 10 15	
AGC TTG CTT CTG ACG CCT TGT GGA TTA GCC TGT GGT CCT GGT AGA GGT	96
Ser Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly	
20 25 30	
TAT GGA AAA CGA AGA CAC CCA AAG AAA TTA ACC CCG TTG GCT TAC AAG	144
Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
35 40 45	
CAA TTC ATC CCC AAC GTT GCT GAG AAA ACG CTT GGA GCC AGC GGC AAA	192
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys	
50 55 60	
TAC GAA GGC AAA ATC ACA AGG AAT TCA GAG AGA TTT AAA GAG CTG ATT	240
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile	
65 70 75 80	
CCG AAT TAT AAT CCC GAT ATC ATC TTT AAG GAC GAG GAA AAC ACA AAC	288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn	
85 90 95	
GCT GAC AGG CTG ATG ACC AAG CGC TGT AAG GAC AAG TTA AAT TCG TTG	336
Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu	
100 105 110	
GCC ATA TCC GTC ATG AAC CAC TGG CCC GGC GTG AAA CTG CGC GTC ACT	384
Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr	
115 120 125	
GAA GGC TGG GAT GAG GAT GGT CAC CAT TTA GAA GAA TCT TTG CAC TAT	432
Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr	
130 135 140	
GAG GGA CGG GCA GTG GAC ATC ACT ACC TCA GAC AGG GAT AAA AGC AAG	480
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys	
145 150 155 160	
TAT GGG ATG CTA TCC AGG CTT GCA GTG GAG GCA GGA TTC GAC TGG GTC	528
Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
165 170 175	
TAT TAT GAA TCT AAA GCC CAC ATA CAC TGC TCT GTC AAA GCA GAA AAT	576
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
180 185 190	
TCA GTG GCT GCT AAA TCA GGA GGA TGT TTT CCT GGG TCT GGG ACG GTG	624
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val	

	195	200	205	
5	ACA CTT GGT GAT GGG ACG AGG AAA CCC ATC AAA GAT CTT AAA GTG GGC Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly 210 215 220			672
10	GAC CGG GTT TTG GCT GCA GAC GAG AAG GGA AAT GTC TTA ATA AGC GAC Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp 225 230 235			720
15	TTT ATT ATG TTT ATA GAC CAC GAT CCG ACA ACG AGA AGG CAA TTC ATC Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile 245 250 255			768
20	GTC ATC GAG ACG TCA GAA CCT TTC ACC AAG CTC ACC CTC ACT GCC GCG Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala 260 265 270			816
25	CAC CTA GTT TTC GTT GGA AAC TCT TCA GCA GCT TCG GGT ATA ACA GCA His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala 275 280 285			864
30	ACA TTT GCC AGC AAC GTG AAG CCT GGA GAT ACA GTT TTA GTG TGG GAA Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu 290 295 300			912
35	GAC ACA TGC GAG AGC CTC AAG AGC GTT ACA GTG AAA AGG ATT TAC ACT Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr 305 310 315 320			960
40	GAG GAG CAC GAG GGC TCT TTT GCG CCA GTC ACC GCG CAC GGA ACC ATA Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile 325 330 335			1008
45	ATA GTG GAT CAG GTG TTG GCA TCG TGC TAC GCG GTC ATT GAG AAC CAC Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His 340 345 350			1056
50	AAA TGG GCA CAT TGG GCT TTT GCG CCG GTC AGG TTG TGT CAC AAG CTG Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu 355 360 365			1104
55	ATG ACG TGG CTT TTT CCG GCT CGT GAA TCA AAC GTC AAT TTT CAG GAG Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu 370 375 380			1152
60	GAT GGT ATC CAC TGG TAC TCA AAT ATG CTG TTT CAC ATC GGC TCT TGG Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp 385 390 395 400			1200
65	CTG CTG GAC AGA GAC TCT TTC CAT CCA CTC GGG ATT TTA CAC TTA AGT Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser 405 410 415			1248
70	TGA			1251

(2) INFORMATION FOR SEQ ID NO:10:

- 60 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 425 amino acids

5 (ii) MOLECULE TYPE: protein

10	Met 1	Val	Glu	Met	Leu 5	Leu	Leu	Thr	Arg	Ile 10	Leu	Leu	Val	Gly	Phe 15	Ile
	Cys	Ala	Leu	Leu 20	Val	Ser	Ser	Gly	Leu 25	Thr	Cys	Gly	Pro	Gly 30	Arg	Gly
15	Ile	Gly	Lys 35	Arg	Arg	His	Pro	Lys 40	Lys	Leu	Thr	Pro	Leu 45	Ala	Tyr	Lys
	Gln	Phe 50	Ile	Pro	Asn	Val	Ala 55	Glu	Lys	Thr	Leu	Gly 60	Ala	Ser	Gly	Arg
20	Tyr 65	Glu	Gly	Lys	Ile	Thr 70	Arg	Asn	Ser	Glu	Arg 75	Phe	Lys	Glu	Leu	Thr 80
	Pro	Asn	Tyr	Asn	Pro 85	Asp	Ile	Ile	Phe	Lys 90	Asp	Glu	Glu	Asn	Thr 95	Gly
25	Ala	Asp	Arg	Leu 100	Met	Thr	Gln	Arg	Cys 105	Lys	Asp	Lys	Leu	Asn 110	Ala	Leu
30	Ala	Ile	Ser 115	Val	Met	Asn	Gln	Trp 120	Pro	Gly	Val	Lys	Leu 125	Arg	Val	Thr
	Glu	Gly 130	Trp	Asp	Glu	Asp	Gly 135	His	His	Ser	Glu	Glu 140	Ser	Leu	His	Tyr
35	Glu 145	Gly	Arg	Ala	Val	Asp 150	Ile	Thr	Thr	Ser	Asp 155	Arg	Asp	Arg	Ser	Lys 160
	Tyr	Gly	Met	Leu 165	Ala	Arg	Leu	Ala	Val	Glu 170	Ala	Gly	Phe	Asp	Trp 175	Val
40	Tyr	Tyr	Glu 180	Ser	Lys	Ala	His	Ile 185	His	Cys	Ser	Val	Lys 190	Ala	Glu	Asn
45	Ser	Val	Ala 195	Ala	Lys	Ser	Gly	Gly 200	Cys	Phe	Pro	Gly	Ser 205	Ala	Thr	Val
	His	Leu 210	Glu	His	Gly	Gly	Thr 215	Lys	Leu	Val	Lys	Asp 220	Leu	Ser	Pro	Gly
50	Asp 225	Arg	Val	Leu	Ala	Ala 230	Asp	Ala	Asp	Gly	Arg 235	Leu	Leu	Tyr	Ser	Asp 240
	Phe	Leu	Thr	Phe 245	Leu	Asp	Arg	Met	Asp	Ser 250	Ser	Arg	Lys	Leu	Phe 255	Tyr
55	Val	Ile	Glu	Thr 260	Arg	Gln	Pro	Arg	Ala 265	Arg	Leu	Leu	Leu	Thr 270	Ala	Ala
60	His	Leu 275	Leu	Phe	Val	Ala	Pro	Gln 280	His	Asn	Gln	Ser	Glu 285	Ala	Thr	Gly

	Ser	Thr	Ser	Gly	Gln	Ala	Leu	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Gln
	290						295					300				
5	Arg	Val	Tyr	Val	Leu	Gly	Glu	Gly	Gly	Gln	Gln	Leu	Leu	Pro	Ala	Ser
	305					310					315					320
	Val	His	Ser	Val	Ser	Leu	Arg	Glu	Glu	Ala	Ser	Gly	Ala	Tyr	Ala	Pro
					325					330					335	
10	Leu	Thr	Ala	Gln	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys
				340					345					350		
15	Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro
			355					360					365			
	Phe	Arg	Leu	Ala	Gln	Gly	Leu	Leu	Ala	Ala	Leu	Cys	Pro	Asp	Gly	Ala
	370						375					380				
20	Ile	Pro	Thr	Ala	Ala	Thr	Thr	Thr	Thr	Gly	Ile	His	Trp	Tyr	Ser	Arg
	385					390					395					400
	Leu	Leu	Tyr	Arg	Ile	Gly	Ser	Trp	Val	Leu	Asp	Gly	Asp	Ala	Leu	His
					405					410					415	
25	Pro	Leu	Gly	Met	Val	Ala	Pro	Ala	Ser							
				420					425							
30	(2) INFORMATION FOR SEQ ID NO:11:															
	(i) SEQUENCE CHARACTERISTICS:															
	(A) LENGTH: 396 amino acids															
	(B) TYPE: amino acid															
35	(D) TOPOLOGY: linear															
	(ii) MOLECULE TYPE: protein															
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:															
	Met	Ala	Leu	Pro	Ala	Ser	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu
	1				5					10					15	
45	Ala	Leu	Ser	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
				20					25					30		
50	Arg	Arg	Tyr	Val	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
			35					40					45			
	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
		50					55					60				
55	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
	65					70					75					80
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
					85					90					95	
60	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile

	100	105	110
	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly		
	115	120	125
5	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly		
	130	135	140
10	Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly		
	145	150	155
	Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr		
	165	170	175
15	Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu		
	180	185	190
	Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu		
	195	200	205
20	Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp		
	210	215	220
25	Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu		
	225	230	235
	Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val		
	245	250	255
30	Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu		
	260	265	270
	Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro		
	275	280	285
35	Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly		
	290	295	300
40	Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu		
	305	310	315
	Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val		
	325	330	335
45	Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp		
	340	345	350
	Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala		
	355	360	365
50	Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser		
	370	375	380
55	Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly		
	385	390	395

(2) INFORMATION FOR SEQ ID NO:12:

60 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 411 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

10 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu  
1 5 10 15  
Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg  
20 25 30  
15 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala  
35 40 45  
20 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser  
50 55 60  
Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu  
65 70 75 80  
25 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn  
85 90 95  
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn  
100 105 110  
30 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg  
115 120 125  
35 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu  
130 135 140  
His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg  
145 150 155 160  
40 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp  
165 170 175  
Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser  
180 185 190  
45 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala  
195 200 205  
50 Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys  
210 215 220  
Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe  
225 230 235 240  
55 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala  
245 250 255  
Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr  
260 265 270  
60 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala

275 280 285

5 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val  
290 295 300

Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val  
305 310 315 320

10 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly  
325 330 335

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala  
340 345 350

15 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro  
355 360 365

Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr  
370 375 380

20 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr  
385 390 395 400

25 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser  
405 410

(2) INFORMATION FOR SEQ ID NO:13:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 437 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser  
1 5 10 15

45 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly  
20 25 30

Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe  
35 40 45

50 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu  
50 55 60

55 Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn  
65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp  
85 90 95

60 Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile  
100 105 110

05827110-040504



Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly  
 115 120 125  
 5 Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly  
 130 135 140  
 Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly  
 145 150 155 160  
 10 Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr  
 165 170 175  
 Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val  
 180 185 190  
 Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu  
 195 200 205  
 20 Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg  
 210 215 220  
 Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu  
 225 230 235 240  
 25 Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile  
 245 250 255  
 Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu  
 260 265 270  
 30 Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser  
 275 280 285  
 Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val  
 290 295 300  
 Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser  
 305 310 315 320  
 40 Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala  
 325 330 335  
 His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val  
 340 345 350  
 45 Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu  
 355 360 365  
 Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly  
 370 375 380  
 Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly  
 385 390 395 400  
 55 Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His  
 405 410 415  
 Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met  
 420 425 430  
 60

115  
 130  
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 415  
 430

Ala Val Lys Ser Ser  
435

5 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 418 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Arg	Leu	Leu	Thr	Arg	Val	Leu	Leu	Val	Ser	Leu	Leu	Thr	Leu	Ser
1				5					10					15	
Leu	Val	Val	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Tyr	Gly	Arg
			20					25					30		
Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile
		35					40					45			
Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly
	50					55					60				
Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr
65				70					75					80	
Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg
			85					90						95	
Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser
			100					105					110		
Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp
	115					120						125			
Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg
	130					135					140				
Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr
145					150					155				160	
Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu
			165					170						175	
Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala
			180					185					190		
Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Leu	Val	Ser	Leu	Gln
	195						200					205			
Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val
	210					215					220				
Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met
225					230					235					240

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	50					55					60					
	Lys 65	Ile	Ser	Arg	Asn	Ser 70	Glu	Arg	Phe	Lys	Glu 75	Leu	Thr	Pro	Asn	Tyr 80
5	Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg
10	Leu	Met	Thr	Gln 100	Arg	Cys	Lys	Asp	Lys 105	Leu	Asn	Ala	Leu	Ala 110	Ile	Ser
	Val	Met	Asn 115	Gln	Trp	Pro	Gly	Val 120	Lys	Leu	Arg	Val	Thr 125	Glu	Gly	Trp
15	Asp	Glu 130	Asp	Gly	His	His	Ser 135	Glu	Glu	Ser	Leu	His 140	Tyr	Glu	Gly	Arg
20	Ala 145	Val	Asp	Ile	Thr	Thr 150	Ser	Asp	Arg	Asp	Arg 155	Ser	Lys	Tyr	Gly	Met 160
	Leu	Ala	Arg	Leu	Ala 165	Val	Glu	Ala	Gly	Phe	Asp 170	Trp	Val	Tyr	Tyr 175	Glu
25	Ser	Lys	Ala	His 180	Ile	His	Cys	Ser	Val 185	Lys	Ala	Glu	Asn	Ser 190	Val	Ala
	Ala	Lys	Ser 195	Gly	Gly	Cys	Phe	Pro 200	Gly	Ser	Ala	Thr	Val 205	His	Leu	Glu
30	Gln	Gly 210	Gly	Thr	Lys	Leu	Val 215	Lys	Asp	Leu	Ser	Pro 220	Gly	Asp	Arg	Val
35	Leu 225	Ala	Ala	Asp	Asp	Gln 230	Gly	Arg	Leu	Leu	Tyr 235	Ser	Asp	Phe	Leu	Thr 240
	Phe	Leu	Asp	Arg	Asp 245	Asp	Gly	Ala	Lys	Lys 250	Val	Phe	Tyr	Val	Ile 255	Glu
40	Thr	Arg	Glu	Pro 260	Arg	Glu	Arg	Leu	Leu 265	Leu	Thr	Ala	Ala	His 270	Leu	Leu
	Phe	Val	Ala 275	Pro	His	Asn	Asp	Ser 280	Ala	Thr	Gly	Glu	Pro 285	Glu	Ala	Ser
45	Ser	Gly 290	Ser	Gly	Pro	Pro	Ser 295	Gly	Gly	Ala	Leu	Gly 300	Pro	Arg	Ala	Leu
50	Phe 305	Ala	Ser	Arg	Val	Arg 310	Pro	Gly	Gln	Arg	Val 315	Tyr	Val	Val	Ala	Glu 320
	Arg	Asp	Gly	Asp	Arg 325	Arg	Leu	Leu	Pro	Ala 330	Ala	Val	His	Ser	Val 335	Thr
55	Leu	Ser	Glu	Glu 340	Ala	Ala	Gly	Ala	Tyr 345	Ala	Pro	Leu	Thr	Ala 350	Gln	Gly
	Thr	Ile	Leu 355	Ile	Asn	Arg	Val	Leu 360	Ala	Ser	Cys	Tyr	Ala 365	Val	Ile	Glu
60	Glu	His 370	Ser	Trp	Ala	His	Arg 375	Ala	Phe	Ala	Pro	Phe 380	Arg	Leu	Ala	His

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	165	170	175
	Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser		
	180	185	190
5	Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala		
	195	200	205
10	Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg		
	210	215	220
	Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe		
	225	230	235
15	Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala		
	245	250	255
	Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr		
	260	265	270
20	Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala		
	275	280	285
	Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val		
	290	295	300
25	Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val		
	305	310	315
30	Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly		
	325	330	335
	Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala		
	340	345	350
35	Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His		
	355	360	365
	Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr		
	370	375	380
40	Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser		
	385	390	395
45	Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser		
	405	410	

(2) INFORMATION FOR SEQ ID NO:17:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 396 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

60	Met	Ala	Leu	Leu	Thr	Asn	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu
	1				5				10					15		

	Ala	Leu	Pro	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
				20					25					30		
5	Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
			35					40					45			
	Val	Pro	Gly	Val	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
		50					55					60				
10	Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
	65					70					75					80
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
					85					90					95	
15	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile
				100					105					110		
	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
20			115					120					125			
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
	130						135					140				
25	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
	145					150					155					160
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
					165					170					175	
30	Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
				180					185					190		
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
35			195					200					205			
	Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
	210						215					220				
40	Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
	225					230					235					240
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
					245					250					255	
45	Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
				260					265					270		
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro
50			275					280					285			
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly
		290					295					300				
55	Gly	Asp	Ala	Leu	Arg	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu
	305					310					315					320
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val
					325					330					335	
60	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp

340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala  
355 360 365

5 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser  
370 375 380

10 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly  
385 390 395

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 416 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

25 Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile  
1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly  
20 25 30

30 Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys  
35 40 45

35 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys  
50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile  
65 70 75 80

40 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn  
85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu  
100 105 110

45 Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr  
115 120 125

50 Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr  
130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys  
145 150 155 160

55 Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val  
165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn  
180 185 190

60 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val

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195 200 205

5 Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly  
210 215 220

10 Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp  
225 230 235 240

Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile  
245 250 255

15 Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala  
260 265 270

His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala  
275 280 285

20 Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu  
290 295 300

Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr  
305 310 315 320

25 Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile  
325 330 335

Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His  
340 345 350

30 Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu  
355 360 365

35 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu  
370 375 380

Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp  
385 390 395 400

40 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser  
405 410 415

(2) INFORMATION FOR SEQ ID NO:19:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1416 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..1413

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG GAT AAC CAC AGC TCA GTG CCT TGG GCC AGT GCC GCC AGT GTC ACC

	Met 1	Asp	Asn	His	Ser 5	Ser	Val	Pro	Trp	Ala 10	Ser	Ala	Ala	Ser	Val 15	Thr	
5	TGT Cys	CTC Leu	TCC Ser	CTG Leu 20	GGA Gly	TGC Cys	CAA Gln	ATG Met	CCA Pro 25	CAG Gln	TTC Phe	CAG Gln	TTC Phe	CAG Gln 30	TTC Phe	CAG Gln	96
10	CTC Leu	CAA Gln	ATC Ile 35	CGC Arg	AGC Ser	GAG Glu	CTC Leu	CAT His 40	CTC Leu	CGC Arg	AAG Lys	CCC Pro	GCA Ala 45	AGA Arg	AGA Arg	ACG Thr	144
15	CAA Gln	ACG Thr 50	ATG Met	CGC Arg	CAC His	ATT Ile	GCG Ala 55	CAT His	ACG Thr	CAG Gln	CGT Arg	TGC Cys 60	CTC Leu	AGC Ser	AGG Arg	CTG Leu	192
20	ACC Thr 65	TCT Ser	CTG Leu	GTG Val	GCC Ala	CTG Leu 70	CTG Leu	CTG Leu	ATC Ile	GTC Val	TTG Leu 75	CCG Pro	ATG Met	GTC Val	TTT Phe	AGC Ser 80	240
25	CCG Pro	GCT Ala	CAC His	AGC Ser	TGC Cys 85	GGT Gly	CCT Pro	GGC Gly	CGA Arg	GGA Gly 90	TTG Leu	GGT Gly	CGT Arg	CAT His	AGG Arg 95	GCG Ala	288
30	CGC Arg	AAC Asn	CTG Leu 100	TAT Tyr	CCG Pro	CTG Leu	GTC Val	CTC Leu	AAG Lys 105	CAG Gln	ACA Thr	ATT Ile	CCC Pro	AAT Asn 110	CTA Leu	TCC Ser	336
35	GAG Glu	TAC Tyr	ACG Thr 115	AAC Asn	AGC Ser	GCC Ala	TCC Ser	GGA Gly 120	CCT Pro	CTG Leu	GAG Glu	GGT Gly	GTG Val 125	ATC Ile	CGT Arg	CGG Arg	384
40	GAT Asp	TCG Ser 130	CCC Pro	AAA Lys	TTC Phe	AAG Lys	GAC Asp 135	CTC Leu	GTG Val	CCC Pro	AAC Asn	TAC Tyr 140	AAC Asn	AGG Arg	GAC Asp	ATC Ile	432
45	CTT Leu 145	TTC Phe	CGT Arg	GAC Asp	GAG Glu	GAA Glu 150	GGC Gly	ACC Thr	GGA Gly	GCG Ala	GAT Asp 155	GGC Gly	TTG Leu	ATG Met	AGC Ser	AAG Lys 160	480
50	CGC Arg	TGC Cys	AAG Lys	GAG Glu	AAG Lys 165	CTA Leu	AAC Asn	GTG Val	CTG Leu 170	GCC Ala	TAC Tyr	TCG Ser	GTG Val	ATG Met	AAC Asn 175	GAA Glu	528
55	TGG Trp	CCC Pro	GGC Gly 180	ATC Ile	CGG Arg	CTG Leu	CTG Leu	GTC Val	ACC Thr 185	GAG Glu	AGC Ser	TGG Trp	GAC Asp 190	GAG Glu	GAC Asp	TAC Tyr	576
60	CAT His	CAC His	GGC Gly 195	CAG Gln	GAG Glu	TCG Ser	CTC Leu	CAC His 200	TAC Tyr	GAG Glu	GGC Gly	CGA Arg	GCG Ala 205	GTG Val	ACC Thr	ATT Ile	624
65	GCC Ala 210	ACC Thr	TCC Ser	GAT Asp	CGC Arg	GAC Asp	CAG Gln 215	TCC Ser	AAA Lys	TAC Tyr	GGC Gly	ATG Met 220	CTC Leu	GCT Ala	CGC Arg	CTG Leu	672
70	GCC Ala 225	GTC Val	GAG Glu	GCT Ala	GGA Gly	TTC Phe 230	GAT Asp	TGG Trp	GTC Val	TCC Ser	TAC Tyr 235	GTC Val	AGC Ser	AGG Arg	CGC Arg	CAC His 240	720
75	ATC Ile	TAC Tyr	TGC Cys	TCC Ser	GTC Val	AAG Lys	TCA Ser	GAT Asp	TCG Ser	TCG Ser	ATC Ile	AGT Ser	TCC Ser	CAC His	GTG Val	CAC His	768

[illegible]

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

10	Met	Asp	Asn	His	Ser	Ser	Val	Pro	Trp	Ala	Ser	Ala	Ala	Ser	Val	Thr
	1				5					10					15	
	Cys	Leu	Ser	Leu	Gly	Cys	Gln	Met	Pro	Gln	Phe	Gln	Phe	Gln	Phe	Gln
				20					25					30		
15	Leu	Gln	Ile	Arg	Ser	Glu	Leu	His	Leu	Arg	Lys	Pro	Ala	Arg	Arg	Thr
			35					40					45			
	Gln	Thr	Met	Arg	His	Ile	Ala	His	Thr	Gln	Arg	Cys	Leu	Ser	Arg	Leu
		50					55					60				
20	Thr	Ser	Leu	Val	Ala	Leu	Leu	Leu	Ile	Val	Leu	Pro	Met	Val	Phe	Ser
	65					70					75					80
25	Pro	Ala	His	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Arg	His	Arg	Ala
					85					90					95	
	Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser
				100					105					110		
30	Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg
			115					120					125			
	Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile
		130					135					140				
	Leu	Phe	Arg	Asp	Glu	Glu	Gly	Thr	Gly	Ala	Asp	Gly	Leu	Met	Ser	Lys
		145				150					155					160
40	Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn	Glu
					165					170					175	
	Trp	Pro	Gly	Ile	Arg	Leu	Leu	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp	Tyr
				180					185					190		
45	His	His	Gly	Gln	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Thr	Ile
			195					200					205			
	Ala	Thr	Ser	Asp	Arg	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu
		210					215					220				
	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Ser	Tyr	Val	Ser	Arg	Arg	His
		225				230					235					240
55	Ile	Tyr	Cys	Ser	Val	Lys	Ser	Asp	Ser	Ser	Ile	Ser	Ser	His	Val	His
					245					250					255	
	Gly	Cys	Phe	Thr	Pro	Glu	Ser	Thr	Ala	Leu	Leu	Glu	Ser	Gly	Val	Arg
				260					265					270		
60	Lys	Pro	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Asp	Arg	Val	Leu	Ser	Met	Thr

[REDACTED]

Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys  
50 55 60

5 Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys  
65 70 75 80

Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly  
85 90 95

10 Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa  
100 105 110

Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser  
115 120 125

15 Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu  
130 135 140

20 Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys  
145 150 155 160

Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe  
165 170 175

25 Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa Gly Gly Xaa Lys Xaa Val  
180 185 190

Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly  
195 200 205

30 Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg  
210 215 220

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 167 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys  
1 5 10 15

Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu  
20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa  
35 40 45

60 Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile  
50 55 60

5 Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg  
65 70 75 80

10 Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp  
85 90 95

15 Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His  
100 105 110

20 His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr  
115 120 125

Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala  
130 135 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa  
145 150 155 160

His Xaa Ser Val Lys Xaa Xaa  
165

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